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RAW SEQUENCE LISTING

DATE: 11/29/2000

PATENT APPLICATION: US/09/712,142

TIME: 09:13:47

Input Set : A:\seqlist 1488 0630002.txt

Output Set: N:\CRF3\11292000\I712142.raw

5 <110> APPLICANT: Ebner, Reinhard
 7 Chopra, Arvind
 9 Ruben, Steven M.
 13 <120> TITLE OF INVENTION: Connective Tissue Growth Factor-3
 17 <130> FILE REFERENCE: 1488.0630002
 C--> 21 <140> CURRENT APPLICATION NUMBER: US/09/712,142
 C--> 21 <141> CURRENT FILING DATE: 2000-11-15
 21 <150> PRIOR APPLICATION NUMBER: US 60/030,720
 23 <151> PRIOR FILING DATE: 1996-11-08
 27 <150> PRIOR APPLICATION NUMBER: US 08/966,020
 29 <151> PRIOR FILING DATE: 1997-11-07
 33 <160> NUMBER OF SEQ ID NOS: 13
 37 <170> SOFTWARE: PatentIn version 3.0
 41 <210> SEQ ID NO: 1
 43 <211> LENGTH: 1285
 45 <212> TYPE: DNA
 47 <213> ORGANISM: Homo sapiens
 51 <220> FEATURE:
 53 <221> NAME/KEY: CDS
 55 <222> LOCATION: (9)..(758)
 59 <220> FEATURE:
 61 <221> NAME/KEY: sig_peptide
 63 <222> LOCATION: (9)..(65)
 67 <220> FEATURE:
 69 <221> NAME/KEY: mat_peptide
 71 <222> LOCATION: (66)..()
 75 <400> SEQUENCE: 1
 76 caggggac atg aga ggc aca ccg aag acc cac ctc ctg gcc ttc tcc ctc 50
 77 Met Arg Gly Thr Pro Lys Thr His Leu Leu Ala Phe Ser Leu
 78 -15 -10
 80 ctc tgc ctc ctc tca aag gtg cgt acc cag ctg tgc ccg aca cca tgt 98
 81 Leu Cys Leu Leu Ser Lys Val Arg Thr Gln Leu Cys Pro Thr Pro Cys
 82 -5 -1 1 5 10
 84 acc tgc ccc tgg cca cct ccc cga tgc ccg ctg gga gta ccc ctg gtg 146
 85 Thr Cys Pro Trp Pro Pro Pro Arg Cys Pro Leu Gly Val Pro Leu Val
 86 15 20 25
 88 ctg gat ggc tgt ggc tgc tgc ccg gta tgt gca ccg ccg ctg ggg gag 194
 89 Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu
 90 30 35 40
 92 ccc tgc gac caa ctc cac gtc tgc gac gcc agc cag gcc ctg gtc tgc 242
 93 Pro Cys Asp Gln Leu His Val Cys Asp Ala Ser Gln Gly Leu Val Cys
 94 45 50 55
 96 cag ccc ggg gca gga ccc ggt gcc ccg ggg gcc ctg tgc ctc ttg gca 290
 97 Gln Pro Gly Ala Gly Pro Gly Gly Arg Gly Ala Leu Cys Leu Leu Ala
 98 60 65 70 75
 100 gag gac gac agc agc tgt gag gtg aac gcc cgc ctg tat ccg gaa ggg 338
 101 Glu Asp Asp Ser Ser Cys Glu Val Asn Gly Arg Leu Tyr Arg Glu Gly

ENTERED

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102      80      85      90
104 gag acc ttc cag ccc cac tgc agc atc cgc tgc cgc tgc gag gac ggc 386
105 Glu Thr Phe Gln Pro His Cys Ser Ile Arg Cys Arg Cys Glu Asp Gly
106      95      100      105
108 ggc ttc acc tgc gtg ccg ctg tgc agc gag gat gtg cgg ctg ccc agc 434
109 Gly Phe Thr Cys Val Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser
110      110      115      120
112 tgg gac tgc ccc cac ccc agg agg gtc gag gtc ctg ggc aag tgc tgc 482
113 Trp Asp Cys Pro His Pro Arg Arg Val Glu Val Leu Gly Lys Cys Cys
114      125      130      135
116 cct gag tgg gtg tgc ggc caa gga ggg gga ctg ggg acc cag ccc ctt 530
117 Pro Glu Trp Val Cys Gly Gln Gly Gly Leu Gly Thr Gln Pro Leu
118      140      145      150      155
120 cca gcc caa gga ccc cag ttt tct ggc ctt gtc tct tcc ctg ccc cct 578
121 Pro Ala Gln Gly Pro Gln Phe Ser Gly Leu Val Ser Ser Leu Pro Pro
122      160      165      170
124 ggt gtc ccc tgc cca gaa tgg agc acg gcc tgg gga ccc tgc tcy acc 626
125 Gly Val Pro Cys Pro Glu Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr
126      175      180      185
128 acc tgt ggg ctg ggc atg gcc acc cgg gtg tcc aac cag aac cgc ttc 674
129 Thr Cys Gly Leu Gly Met Ala Thr Arg Val Ser Asn Gln Asn Arg Phe
130      190      195      200
132 tgc cga ctg gag acc cag cgc cgc ctg tgc ctg tcc agg ccc tgc cca 722
133 Cys Arg Leu Glu Thr Gln Arg Arg Leu Cys Leu Ser Arg Pro Cys Pro
134      205      210      215
136 ccc tcc agg ggt cgc agt cca caa aac agt gcc ttc tagagccggg 768
137 Pro Ser Arg Gly Arg Ser Pro Gln Asn Ser Ala Phe
138      220      225      230
140 ctgggaatgg ggacacgggtg tccaccatcc ccagctggtg gccctgtgcc tgggccctgg 828
142 gctgatggaa gatggtccgt gccagggccc ttggtgcag gcaacacttt agcttgggtc 888
144 caccatgcag aacaccaata ttaacacgct gccgtggtctg tctggatccc gaggtatggc 948
146 agaggtgcaa gacctagtcc cctttctctt aactcactgc ctaggaggct ggccaagggtg 1008
148 tccaggggtcc tctagccccc tccctgccta cacacacagc ctatatcaaa catgcacacg 1068
150 ggcgagcttt ctctccgact tcccctgggc aagagatggg acaagcagtc ccttaatat 1128
152 gaggtgcag caggtgctgg gctggactgg ccatttttct gggggtagga tgaagagaag 1188
154 gcacacagag attctggatc tctgctgcc tttctggag tttgtaaaat tgttctgaa 1248
156 tacaagccta tgcgtgaaaa aaaaaaaaaa aaaaaaa 1285
159 <210> SEQ ID NO: 2
161 <211> LENGTH: 250
163 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
169 <400> SEQUENCE: 2
171 Met Arg Gly Thr Pro Lys Thr His Leu Leu Ala Phe Ser Leu Leu Cys
172      -15      -10      -5
175 Leu Leu Ser Lys Val Arg Thr Gln Leu Cys Pro Thr Pro Cys Thr Cys
176      -1 1      5      10
179 Pro Trp Pro Pro Pro Arg Cys Pro Leu Gly Val Pro Leu Val Leu Asp
180      15      20      25
183 Gly Cys Gly Cys Cys Arg Val Cys Ala Arg Arg Leu Gly Glu Pro Cys

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184 30          35          40          45
187 Asp Gln Leu His Val Cys Asp Ala Ser Gln Gly Leu Val Cys Gln Pro
188          50          55          60
191 Gly Ala Gly Pro Gly Gly Arg Gly Ala Leu Cys Leu Leu Ala Glu Asp
192          65          70          75
195 Asp Ser Ser Cys Glu Val Asn Gly Arg Leu Tyr Arg Glu Gly Glu Thr
196          80          85          90
199 Phe Gln Pro His Cys Ser Ile Arg Cys Arg Cys Glu Asp Gly Gly Phe
200          95          100          105
203 Thr Cys Val Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser Trp Asp
204 110          115          120          125
207 Cys Pro His Pro Arg Arg Val Glu Val Leu Gly Lys Cys Cys Pro Glu
208          130          135          140
211 Trp Val Cys Gly Gln Gly Gly Gly Leu Gly Thr Gln Pro Leu Pro Ala
212          145          150          155
215 Gln Gly Pro Gln Phe Ser Gly Leu Val Ser Ser Leu Pro Pro Gly Val
216          160          165          170
219 Pro Cys Pro Glu Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr Thr Cys
220          175          180          185
223 Gly Leu Gly Met Ala Thr Arg Val Ser Asn Gln Asn Arg Phe Cys Arg
224 190          195          200          205
227 Leu Glu Thr Gln Arg Arg Leu Cys Leu Ser Arg Pro Cys Pro Pro Ser
228          210          215          220
231 Arg Gly Arg Ser Pro Gln Asn Ser Ala Phe
232          225          230
235 <210> SEQ ID NO: 3
237 <211> LENGTH: 349
239 <212> TYPE: PRT
241 <213> ORGANISM: Homo sapiens
245 <400> SEQUENCE: 3
247 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
248 1          5          10          15
250 Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
251          20          25          30
253 Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
254          35          40          45
256 Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
257          50          55          60
259 Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
260 65          70          75          80
262 Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
263          85          90          95
265 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
266          100          105          110
268 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
269          115          120          125
271 Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
272          130          135          140
274 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys

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```

275 145          150          155          160
277 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
278          165          170          175
280 Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
281          180          185          190
283 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
284          195          200          205
286 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
287          210          215          220
289 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
290 225          230          235          240
292 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
293          245          250          255
295 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
296          260          265          270
298 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
299          275          280          285
301 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
302          290          295          300
304 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
305 305          310          315          320
307 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
308          325          330          335
310 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
311          340          345
313 <210> SEQ ID NO: 4
315 <211> LENGTH: 36
317 <212> TYPE: DNA
319 <213> ORGANISM: DNA primer
323 <400> SEQUENCE: 4
324 caccacggat ccaaggtgcg tacccagctg tgcccg 36
327 <210> SEQ ID NO: 5
329 <211> LENGTH: 32
331 <212> TYPE: DNA
333 <213> ORGANISM: DNA primer
337 <400> SEQUENCE: 5
338 gatgtaagct tcgtgtcccc attcccagcc cg 32
341 <210> SEQ ID NO: 6
343 <211> LENGTH: 39
345 <212> TYPE: DNA
347 <213> ORGANISM: DNA primer
351 <400> SEQUENCE: 6
352 cggcaggatc cgccatcatg agaggcacac cgaagaccc 39
355 <210> SEQ ID NO: 7
357 <211> LENGTH: 32
359 <212> TYPE: DNA
361 <213> ORGANISM: DNA primer
365 <400> SEQUENCE: 7
366 gatgtggtac ccgtgtcccc attcccagcc cg 32

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Input Set : A:\seqlist 1488 0630002.txt

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369 <210> SEQ ID NO: 8
371 <211> LENGTH: 40
373 <212> TYPE: DNA
375 <213> ORGANISM: DNA primer
379 <400> SEQUENCE: 8
380 gctcggatcc gccatcatga gaggcacacc gaagacccac 40
383 <210> SEQ ID NO: 9
385 <211> LENGTH: 43
387 <212> TYPE: DNA
389 <213> ORGANISM: DNA primer
393 <400> SEQUENCE: 9
394 gatgtttctag aagaaggcac tgtttttgtgg actgcgaccc ctg 43
397 <210> SEQ ID NO: 10
399 <211> LENGTH: 264
401 <212> TYPE: DNA
403 <213> ORGANISM: EST
407 <220> FEATURE:
409 <221> NAME/KEY: Unsure
411 <222> LOCATION: (56)..(56)
413 <223> OTHER INFORMATION: May be any nucleotide.
419 <220> FEATURE:
421 <221> NAME/KEY: Unsure
423 <222> LOCATION: (128)..(128)
425 <223> OTHER INFORMATION: May be any nucleotide.
431 <220> FEATURE:
433 <221> NAME/KEY: Unsure
435 <222> LOCATION: (246)..(246)
437 <223> OTHER INFORMATION: May be any nucleotide.
443 <400> SEQUENCE: 10
OK-> 444 ctggtggccc tgtgctggg ccctgggctg atggaagatg gtccgtgcc aggccnttgg 60
446 ctgcaggcaa-cacttttagct tgggtccacc atgcagaaca ccaatatata cacgctgcct 120
W--> 448 ggtctgtntg gatcccgagg tatggcagag gtgcaagacc tagtctcttt tcctctaact 180
450 caetgcctag gaggetggcc aaggtgtcca gggctctcta gccacttcc tgctacaca 240
452 cacagnctat atcaaacatg caca 264
455 <210> SEQ ID NO: 11
457 <211> LENGTH: 239
459 <212> TYPE: DNA
461 <213> ORGANISM: EST
465 <220> FEATURE:
467 <221> NAME/KEY: Unsure
469 <222> LOCATION: (5)..(5)
471 <223> OTHER INFORMATION: May be any nucleotide.
477 <220> FEATURE:
479 <221> NAME/KEY: Unsure
481 <222> LOCATION: (10)..(10)
483 <223> OTHER INFORMATION: May be any nucleotide.
489 <220> FEATURE:
491 <221> NAME/KEY: Unsure
493 <222> LOCATION: (85)..(85)

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FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/712,142

DATE: 11/29/2000

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Input Set : A:\seqlist 1488 0630002.txt

Output Set: N:\CRF3\11292000\I712142.raw

L:21 M:270 C: Current Application Number differs, Replaced Current Application No
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13